

FIG. 1A

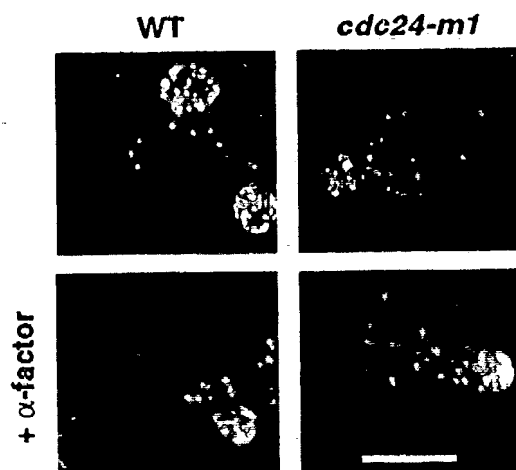


FIG. 1B

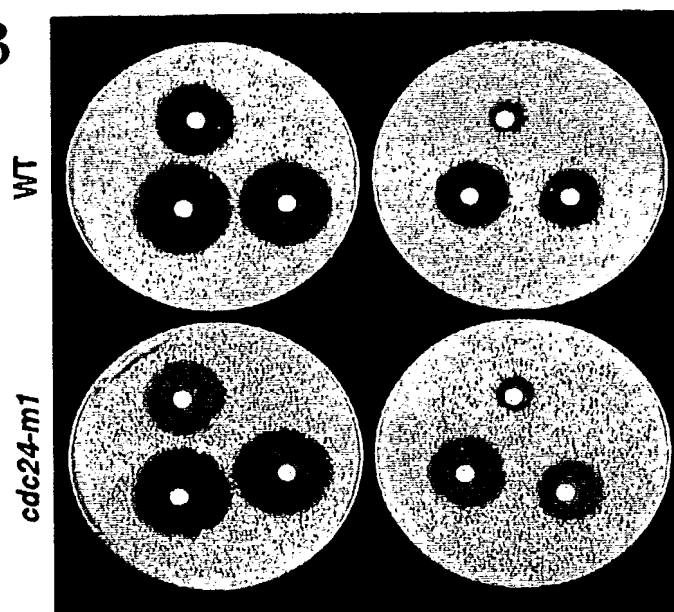
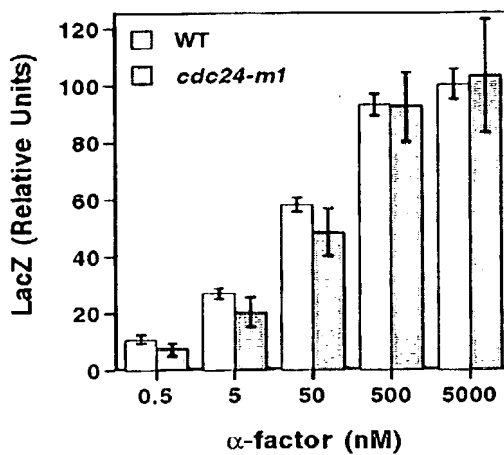


FIG. 1C





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FIG. 2A

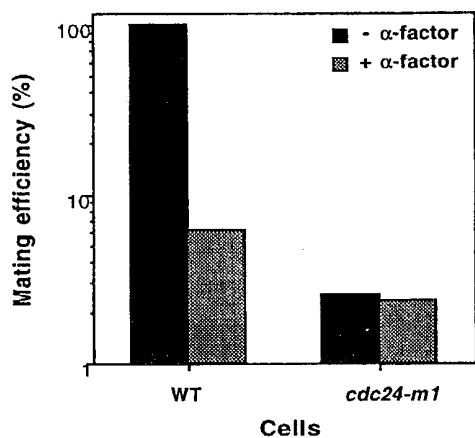


FIG. 2B

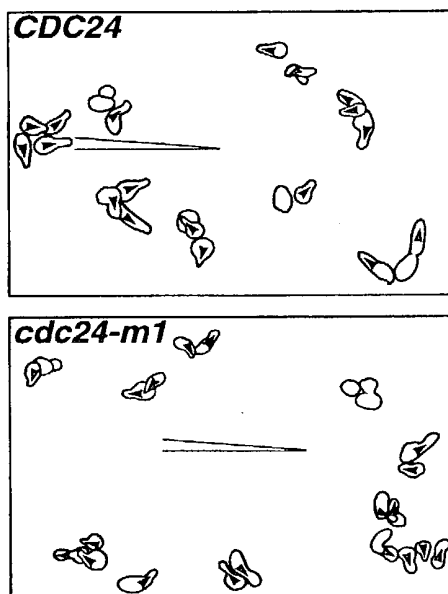


FIG. 2C

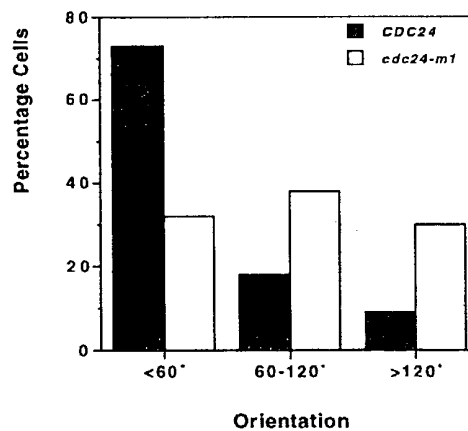
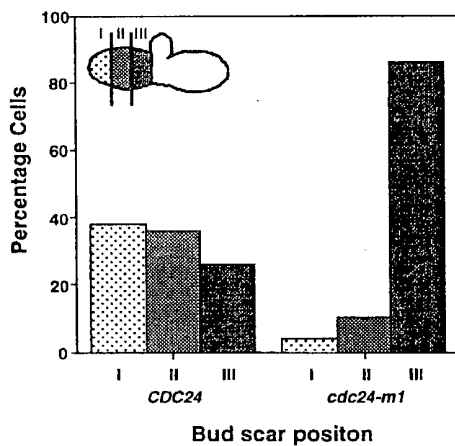


FIG. 3A

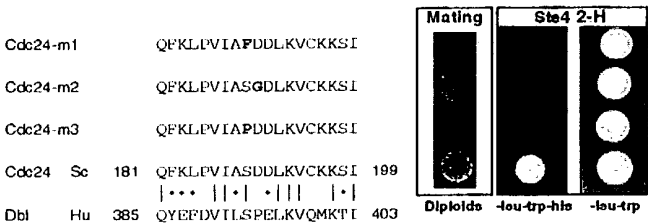


FIG. 3B

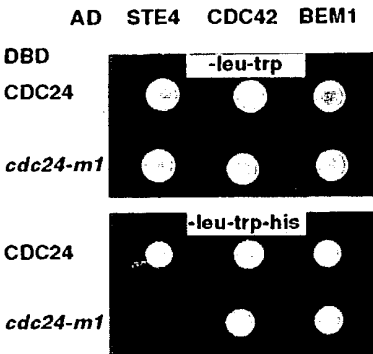


FIG. 3C

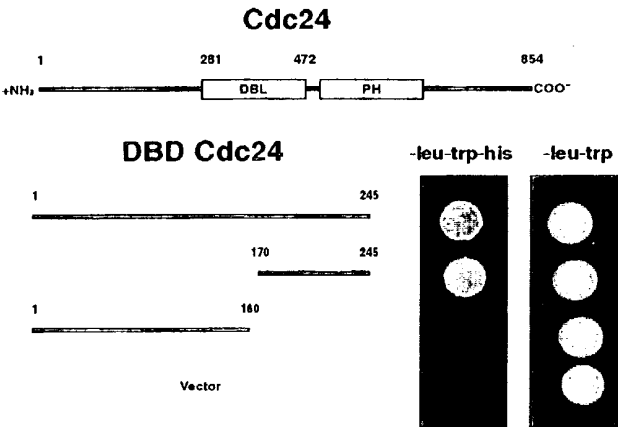
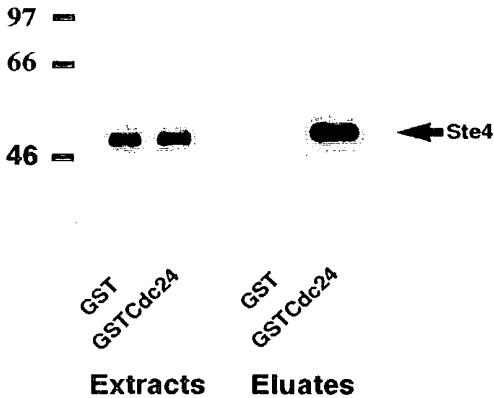


FIG. 3D



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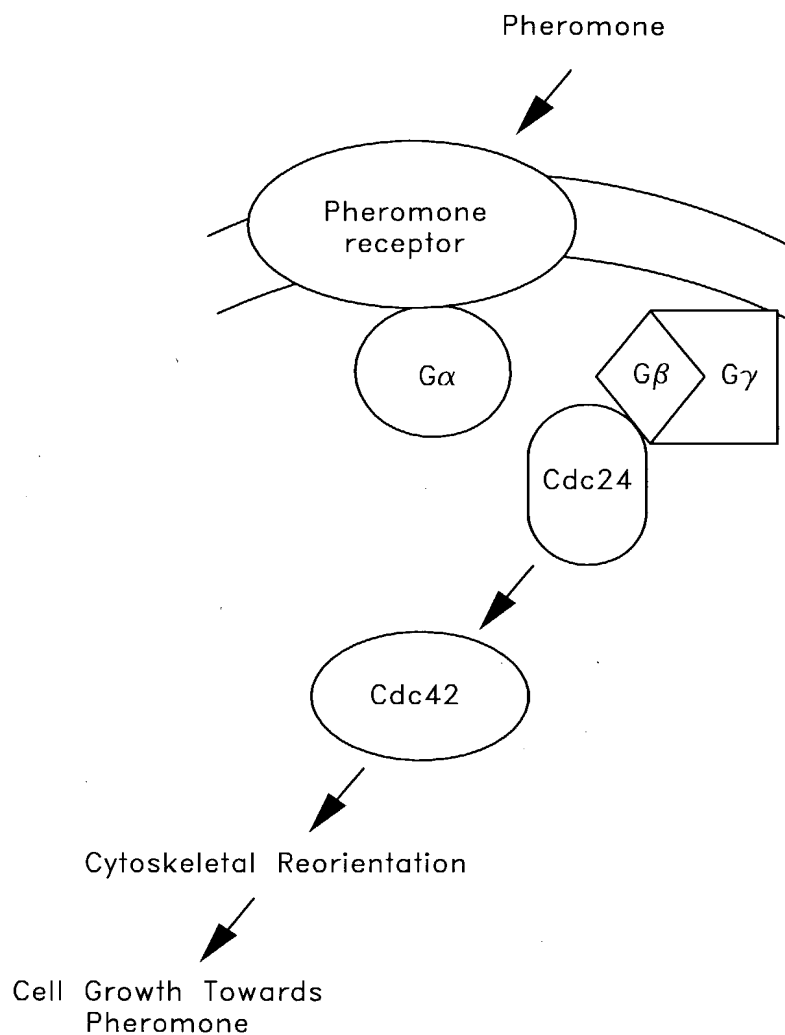


FIG. 4



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 5_A

FIG. 5_B

FIG. 5

NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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5	2113/1	ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA	2143/11	TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT
	M E H P P A A L R T		F S T Q S T S S L N	
10	2173/21	TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT	2203/31	GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT
	S V S T V S S S R I		V S S G P V N I N N	
	2233/41	TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT	2263/51	TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA
	F N K P S T P K D H		L F Y R C E S L K R	
15	2293/61	AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA	2323/71	TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA
	K L Q K I P G M E P		F L N Q A F N Q A E	
	2353/81	CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG	2383/91	GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT
20	Q L S E Q Q A L A L		A Q E R S N G N G H	
	2413/101	AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC	2443/111	GGT GCC ATG AAT AGA CTT TCA GTT GGT TCT
	S N G K R H Q S L D		G A M N R L S V G S	
25	2473/121	GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA	2503/131	CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT
	D S S S I Q G S L T		R M A T N A S T S S	
	2533/141	TTA ATC AGT GGT ATG CCA AAC AAC AAC ACT	2563/151	TTA TTT ACG TTT ACT GCA GGG GTT TTA CCA
30	L I S G M P N N N T		L F T F T A G V L P	
	2593/161	GCT AAT ATT AGT GTC GAT CCT GCT ACC CAT	2623/171	CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC
	A N I S V D P A T H		L W K L F Q Q G A P	
	2653/181	TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT	2683/191	GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT
35	F C V L I N H I L P		D S Q I P V V S S D	
	2713/201	GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT	2743/211	GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG
	D L R I C K K S V Y		D F L I A V K T Q L	
40	2773/221	AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA	2803/231	TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT
	N F D D E N M F T I		S N V F S D N A Q D	
	2833/241	TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA	2863/251	CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC
45	L I K I I D V I N K		L L A E Y S D A S D	
	2893/261	CTG GGT GGT GGC GAT GAA GAT GTA AAT ATG	2923/271	GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA
	S G G G D E D V N M		D V Q I T D E R S K	
	2953/281	GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA	2983/291	AAA TAT GTT CAA GAC TTG GAA CTA ATG TGT
50	V F R E I I E T E R		K Y V Q D L E L M C	
	3013/301	AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA	3043/311	AAT TTG TCT TCA GAA CAA ATT CAC TTG TTA
	K Y R Q D L I E A E		N L S S E Q I H L L	
	3073/321	TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT	3103/331	CAA AGA CGA TTC CTC AAT GGG TTA GAA TGT
55	F P N L N E I I D F		Q R R F L N G L E C	
	3133/341	AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA	3163/351	ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG
60	N I N V P I R Y Q R		I G S V F I H A S L	
	3193/361	GGC CCT TTC AAT GCT TAT GAA CCT TGG ACT	3223/371	ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC
	G P F N A Y E P W T		I G Q L T A I D L I	
	3253/381	AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG	3283/391	TCA AGT CTA CTT GAT CCT GGG TTT GAA CTT
65	N K E A A N L K K S		S S L L D P G F E L	
	3313/401	CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA	3343/411	TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG
	Q S Y I L K P I Q R		L C K Y P L L L K E	
	3373/421	TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA	3403/431	CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA
70	L I K T S P E Y S K		Q D P H G S S S S T	
	3433/441	TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT	3463/451	GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT
	S F N E L L V A K T		A M K E L A N Q V N	

FIG. 5A



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	3493/461	GAG GCG CAA AGA CGA GCA GAA AAT ATC GAA	3523/471	CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT
	E A Q R R A E N I E	H L E K L K E R V G		
5	3553/481	AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA	3583/491	GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG
	N W R G F N L D A Q	G E L L F H G Q V G		
	3613/501	GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC	3643/511	GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT
	V K D A E N E K E Y	V A Y L F E K I V F		
10	3673/521	TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA	3703/531	TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT
	F F T E I D D T K K	S D K Q E K K S K F		
	3733/541	TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT	3763/551	CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA
15	S T R K R S T S S N	L S S S T T N L L E		
	3793/561	TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA	3823/571	TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT
	S I N N S R K D N T	L P L E L K G R V Y		
20	3853/581	ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA	3883/591	AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA
	I S E I Y N I S A P	N T P G S T L I I S		
	3913/601	TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC	3943/611	ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA
	W S G R K E S G S F	T L R Y R S E E A R		
25	3973/621	AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG	4003/631	AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT
	N Q W E K C L R D L	K T N E M N K Q I H		
	4033/641	AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT	4063/651	AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC
30	K K L R D S D S S F	N T D D S A I Y D Y		
	4093/661	ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA	4123/671	TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG
	T G I S T S P V N Q	S T Q Q Q Y Y D H R		
35	4153/681	GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG	4183/691	TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT
	G S H S S R H H S S	S S T L S M M K N N		
	4213/701	AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA	4243/711	TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC
	R V K S G D L S R I	S S T S T L D S F		
40	4273/721	AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC	4303/731	ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC
	S N N L N G S P N T	T N P S L M S S D A		
	4333/741	ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA	4363/751	ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG
45	T K T I P T F D V A	I K L L Y K S T E L		
	4393/761	TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT	4423/771	GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC
	S E P L I V N A Q I	E Y N D L L Q K I I		
50	4453/781	TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA	4483/791	GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT
	S Q I I T S N L V A	D D V N I S R L R Y		
	4513/801	AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG	4543/811	AAT TCA GAT GAT GAT TGG GGG TTA GTG CTT
	K D D E G D F V N L	N S D D D W G L V L		
55	4573/821	GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA	4603/831	ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA
	D M L T S E D F Y Q	T S S N E K R S V T		
	4633/841	GTG TGG GTT TCT TGA		
60	V W V S *			

FIG. 5_B



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1 MAIQ---TR-FA 8
M R F+
C.a. Cdc24p: 1 MEHPPAALRTFSTQ 14

10 S.c. Cdc24p: 9 SGTSLSDLKPKPSATISISIPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPLQPKPFLQL 66
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL
C.a. Cdc24p: 15 STSSLNSVSTVSSSRIVSSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPFLNQ 74

15 S.c. Cdc24p: 67 AYQSSEVLSEKQSLLSQKQHQELLKSNGANRSDSLAP---TLRSSISISTATSLMSMEG 123
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
C.a. Cdc24p: 75 AFNQAEQLSEQALALAQERSNGNGHSGNGKRHSQSLDGAMNRLSVGSDSSSIQGSILTRMAT 134

20 S.c. Cdc24p: 124 ISYTSNPSATPNMEDTLTFTSMGILPITMDCDPVTQSLQFQQGAPLCILFNSVKPOFK 183
+ T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
C.a. Cdc24p: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLQFQQGAPFCILNHILPDSQ 193

S.c. Cdc24p: 184 LPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFNANSTSQLVKVLEVVETLMN 243
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
25 C.a. Cdc24p: 194 IPVVSDDLRIKCKSVYDFLIAVKTQLNFDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

S.c. Cdc24p: 244 SSPTIFPSKSKTQIMNAENQHRHQPOQSSKKHNEYVKIIEFVATERKYVHDLEILDY 303
S + + + +E K+ +E + TERKYV DLE++ KY
C.a. Cdc24p: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIETERKYVQDLELMCKY 302

30 S.c. Cdc24p: 304 RQQLDLSNLTSEELYMLFPLNGDAIDFORRFLISLEINALVEPSKQRIQALFMH-SKHF 362
RQ L+++ ++SE+++LFPNL + IDQRRFL LE N V ORIG++F+H S
C.a. Cdc24p: 303 RQDLIEAENLSSEQIHLFPNLNEIIDQRRFLNGLECNINVPRIYQRIQSVFIHASLGP 362

35 S.c. Cdc24p: 363 FKLYEPWSIGQNAIEFLSSTLHKMRVDESQRFIINNKLQSLYKPVORLCRYPLLVK 422
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
C.a. Cdc24p: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQSYILKPIQLCKYPLLLK 419

S.c. Cdc24p: 423 ELLAE-----SSDDNNTKELEAALDISKNARSINENQRRTENHQVVKLYGRV 471
EL+ SS + EL A K +A +NE QRR EN + ++KL RV
40 C.a. Cdc24p: 420 ELIKTSPEYSKQDPHGSSSSTSFNELLVAKTAMKELANQVNEAQRRAENIEHLEKLKERV 479

S.c. Cdc24p: 472 VNWKGYRISKFGELLYFDKVFISTNNSSEPEREFEVLYFEKIIILFSEVVTKKSASSLI 531
NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +
45 C.a. Cdc24p: 480 GNWRGFNLDAQGELLFHGQVGV---KDAENEKEYVAYLFEKIVFFTEIDDTKKSDKQE 535

S.c. Cdc24p: 532 LKKKSSTASISASNITDNGSPHHSYHKRHSNSSSSNNIHLSSSSAAAIHSSSTNSDN 591
K K ST ++SN+ SSS ++ S NS +
50 C.a. Cdc24p: 536 KSKFPSTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

S.c. Cdc24p: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649
N+ L+L+GR+ I + I N +L I+W KE G+F L+
C.a. Cdc24p: 569 NT-----LPLELKG RVYI SEIYNISAPNTPGSTLIISWSGRKESGSFTLR 613

55 S.c. Cdc24p: 650 FKNEETRDNWSSCLQQLIHLKNEQFKARHHSSTSTSS-----TAKSSMMSPTTT 701
+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T
C.a. Cdc24p: 614 YRSEARNQWEKCLRLDKTNEMNKQIHKLRDSDSSFNDDSAIYDYTGISTSPVNQSTQ 673

S.c. Cdc24p: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS---DVLPKRRTTSSSEFEIKS----- 748
+H S + H S ++ S RV + TT SF + +
60 C.a. Cdc24p: 674 QQYYDHRGSHSSSRHSSSSTLSMMKNRVKSGDLRSISSTSTLDSFNNLNGSPNTTNP 733

S.c. Cdc24p: 749 --ISENFKNSIPESSILFRISYNNNSNNTSSSEIFTLLEKVVNFDDLIMAINSKI--SN 804
+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN
65 C.a. Cdc24p: 734 SLMSSDATKTIPTFDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKTIITSN 787

S.c. Cdc24p: 805 THNNNISPIITKIKYQDEGDGDFVVLGSDSDWNVAKEMLAENNEKFLNIRLY 854
++++ I++++Y+D++GDFV L SD+DW + +ML + F +
C.a. Cdc24p: 788 LVADDVN--ISRLRYKDEGDGDFVNLNSDDDWGLVLDMLTSED--FYQTSSNEKRSVTVWVS 844

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FIG. 6



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FIG. 7A₁

FIG. 7A₂

FIG. 7A



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FIG. 7A₁

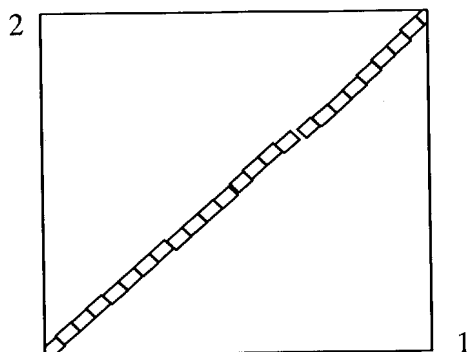
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1 .. 854)

Sequence 2 lcl|C.a. Cdc24p Length 844 (1 .. 844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 446 bits (1136), Expect = e-124
Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)

```
Query: 9  SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLFIHICANIRKRLEVLPLQLKPFLLQL 66
      S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL
Sbjct: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEFPFLNQ 74

Query: 67 AYQSSEVLSEERQSLLLSQKQHQELLKSNGANRDSSDLAP---TLRSSISISTATSLMSMEG 123
      A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
Sbjct: 75 AFNQAEQLSEQQALALAQERSNNGNHSNGKRHSQSLDGAMNRLSVGSDSSSIQGSILTRMAT 134

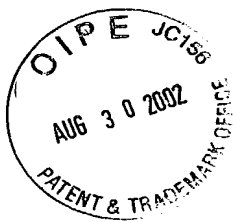
Query: 124 ISYTNNSNPSTPNMEDTLTLTFSMGILPITMDCDPVTQLSQLFQQGAPLCILFNSVKPQFK 183
      + T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
Sbjct: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFQQGAPFCVLINHLIPDSQ 193

Query: 184 LPVIASDDLKVKCKSIYDFILGCKKHFAFNDEELFTISDVFNSTSQLVKVLEVETLMN 243
      +PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
Sbjct: 194 IPVVSDDLRLCKKSVYDFLIAVKTQLNFDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

Query: 244 SSPTIFPSKSKTQQIMNAENQHRHQPPQSSKKHNEYVKIIKEFVATERKYVHDLILDYK 303
      S + + + +E K+ +E + TERKYV DLE++ KY
Sbjct: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIIETERKYVQDLELMCKY 302

Query: 304 RQQLLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQRIGALFMH-SKHF 362
      RQ L+++ ++SE++++LFPNL + IDFQRRFL LE N V QRIQ++F+H S
Sbjct: 303 RQDLIEAENLSSEQIHLLFPNLNEIDFQRRFLNGLECNINVPRIYQRIQSVFIHASLGP 362

Query: 363 PKLYEPWSIGQNAIEFLSSTLHKMRVDESQRFIINNKLELQSFLYKPVQRLCRYPLLVK 422
      F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQSYILKPIQRLCKYPLLLK 419
```



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Query: 551 --NGSPHHSYHKRHSNSSSSNNIHL-----SSSAAAIHSSSTNSSDNNSSNNSSSS 599
G P H + S + + S + I S + + N N SSS
Sbjct: 477 FWRGDPQHESFILKLRNEESHKLWMSVLNRLWKNEHGSPKDIRSAASTPANPVYNRSSS 536

Query: 600 SLFKLSANEPKLD-LRGRIMIMNLN---QIIPQNNRSLNITWESIKEQGNFLLKFKNEET 655
K N D LR + N+N I +++S T + K+ K+ T
Sbjct: 537 QTSK-GYNSSDYDLLRTHSLDENVNSTSISSPSSKSPFTKTTSKDT-----KSATT 588

Query: 656 RDNWSSCLQQLIHDLKNEQFKARHHSSTST-----TSSTAKSSSMMSPPTTMMNT--PNHH 708
D S +L + R +TST +SSTA S +S + +N+ +++
Sbjct: 589 TDERPSDFIRLNSEESVGTSSLRTSQTTSTIVSNDSSSTASIPSQISRISQVNSLLNDYN 648

Query: 709 NSRQTH-----DSMASF---SSSHMKRVSD-----VLPKRRTTSSSFES 745
+RQ+H S++ F SSS +++ D + P++ + S+ +S+
Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708

Query: 746 IKSISENFKNSIPESSILFRISYNNNSNNTSSSEI----FTLLVEKVWNFDDLIMAINSK 801
+ S+ SS +S N +N + L+V FD+L+ + K
Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLHEVSLVLVVAHDITFDELLAKVEHK 768

Query: 802 IS--NTHNNNISPI TKIKYQDEGDGFVVLGSDDEWNVAKE 839
I + ++KY DEDGDF+ + SDED +A E
Sbjct: 769 IKLCGILKQAVPFRVRLKYVDEGDGFITITSDEDEVLMFAFE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.

Gapped

Lambda K H
0.270 0.0470 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 10384

Number of Sequences: 0

Number of extensions: 671

Number of successful extensions: 13

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 834

length of database: 90,077,593

effective HSP length: 61

effective length of query: 773

effective length of database: 83489227

effective search space: 64537172471

effective search space used: 64537172471

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 41 (21.7 bits)

S2: 73 (32.8 bits)

FIG. 7A₂



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 7B₁

FIG. 7B₂

FIG. 7B



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FIG. 7B₁

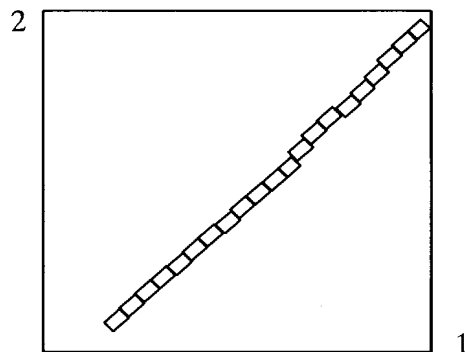
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

Sequence 1 lcl|S.c. Cdc24p Length 854 (1 .. 854)

Sequence 2 lcl|S.p. Cdc24p Length 834 (1 .. 834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61

Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)

```
Query: 156 DPVTQLSQLFQQGAPLCILFNSVKPQFKLPVIASDDLK---VCKKSIYDFILGCKKHFAF 212
          DPVT++   + G PLC LFN +   + KL V +S L+   VCK S+Y F+L CK
Sbjct: 67  DPVTEIWLFCRLGYPLCALFNCLPVKQKLEVNSSVSLENTNVCKASLYRFMLMCKKNELGL 126

Query: 213 NDEELFTISDVFANSTSQLVKVLEVETLMNSSPTIFPSKSKTQQIMNAENQHRHQPPQS 272
          D LF+IS+++ ST+ LV+ L+ +E L+   +KS +   + ++   S
Sbjct: 127 TDAALFSISEIYKPSTAPLVRALQTIELLLKKYEVSNTTKSSSTPSPSTDDNVPTGTLNS 186

Query: 273 SKKHNEYVKIIKEFVATERKYVHDLEILDKYRQQLLDSNLITSEELYMLFPNLGDAIDFQ 332
          ++ E   TE KY+ DLE L Y L   +++ + + +F NL + +DFQ
Sbjct: 187 LIASGR--RVTAELYETELKYIQDLEYLSNYMVILQQKQILSQDTILSIFTNLNEILDFO 244

Query: 333 RRFLISLEINALVEPSKQORIGALFMHSHFFKLYEPWSIG-QNAAIEFLSSTLHKMRVDE 391
          RRFL+ LE+N +   +QR+GALF+ + F +Y+ +   NA   + +   ++V
Sbjct: 245 RRFLVGLEMNLSLPVEEQRLGALFIALEEGFSVYQVFCTNFPNAQQLIIDNQNLKLVAN 304

Query: 392 SQRFIINNKLELQSFYLYKPVQRLCRYPLLVKELL-AESSDDNNTKELEAALDISKNIARS 450
          ++   EL + L KP+QR+C+YPLL+ +LL   S   +EL+ +   +A
Sbjct: 305 ----LLEPSYELPALLIKPIQRICKYPLLLNQLLKGTPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRTTENHQVVKLYGRVWNWKGYSRISKFGELLYFDKVFISTNSSSEPEREFEVYL 510
          +NE +R EN   + +L RV++WKGY + FG+LL +D V +   ++ ERE+ VYL
Sbjct: 361 VNETRRIHENRNAIIELEQRVIDWKGYSLQYFGQLLVWDVVNV----CKADIERYHYVL 416

Query: 511 FEKIIILFSEVVT-KKSASSLILKKKSSTSAS-----ISASNITDN----- 550
          FEKI++   E+ T K+ A S+ + KK+   S   I SNIT
Sbjct: 417 FEKILLCKEMSTLKRQARSISMNKKTKRLDSLQKGRILTSNITTVPNHHMGSYAIQI 476
```



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FIG. 7B₂

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Query: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRTENHQVVKLYGRV 471
EL+ SS + EL A K +A +NE QRR EN + ++KL RV
Sbjct: 420 ELIKTSPEYSKQDPHGSSSSSTSPNELLVAKTAMKELANQVNEAQRRAENIEHLEKLKERV 479

Query: 472 VNWKGYRISKFGELLYFDKVFISTTNSSEPEREFEVYLFEKIIILFSEVVTKKSASSLI 531
NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +
Sbjct: 480 GNWRGFNLDAQGELLFHGQVGV-----KDAENEKEYVAYLFEKIVFFFTEIDDTKKSDKQE 535

Query: 532 LKKKSSTASISASNITDNNNGSPHSHYHKRHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591
K K ST ++SN+ SSS ++ S NS +
Sbjct: 536 KSKFSTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

Query: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649
N+ L+L+GR+ I + I N +L I+W KE G+F L+
Sbjct: 569 NT-----LPLELKGRVYISEIYNISAPNTPGSTLIISWSGRKESGSPTLR 613

Query: 650 FKNEETRDNWSSCLQQLIHLKNEQFKARHHSSTSTTSS-----TAKSSSMMSPTTT 701
+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T
Sbjct: 614 YRSEEARNQWEKCLRDLTNEMNKQIHKKLRDSDSSFNTDDSAIYDYGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS----DVLPKRRTTSSSFESIKS----- 748
+H S + H S ++ S RV + TT SF + +
Sbjct: 674 QQYYDHGRSHSRHSSSSTLSMMKNRVRKSGDLSRISSTSTTLDSFSNNLNGSPNTTNP 733

Query: 749 --ISENFKNSIPESSILFRISYNNNSNNTSSSEIPTLLVEKVWNFDDLIMAINSKI--SN 804
+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN
Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY----KSTELSE--PLIVNAQIEYNDLLQKIISQIITSN 787

Query: 805 THNNNISPIITKIKYQDEDGDFVVLGSDDEDWNVAKEMLAENN 845
++++ I++++Y+D++GDFV L SD+DW + +ML +
Sbjct: 788 LVADDVN-ISRLRYKDDEGDFVNLNSDDDWGLVLDMLTSED 827

CPU time: 0.26 user secs. 0.02 sys. secs 0.28 total secs.

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12253

Number of Sequences: 0

Number of extensions: 709

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 844

length of database: 90,077,593

effective HSP length: 63

effective length of query: 781

effective length of database: 83353792

effective search space: 65099311552

effective search space used: 65099311552

T: 9

A: 40

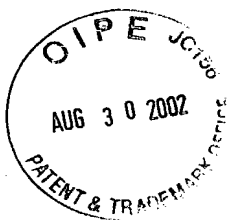
X1: 16 (7.2 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 42 (21.9 bits)

S2: 73 (32.8 bits)



11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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Sc KLPVIASDDLKVCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

Ca QIPVVSSDDLRLCKKSVYDFLI (SEQ ID No 26)

Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

FIG. 8



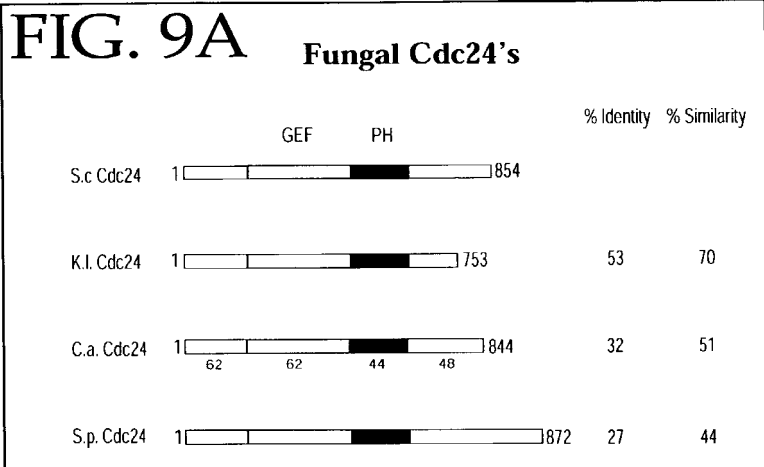
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**FIG. 9B**

Guanine nucleotide exchange factor domain of CaCDC24 is homologous to other fungal Cdc24p's

```

S.c. 227 STSOLVKVLEVVETLMNSSPTIFPSKSKTOQIMNAENQHRHQPQSSKKHNEYVKIIEKF
K.l. 221 STDHFLKVLVDVNTLLNAAEVEFPQIDMSTOLE-----S-QRAKAPQTEYDKIVKEF
C.a. 237 NAQDLIKIIVINKLLAEVSDASDGGGDEDVN-----MDVQITDERSKVFPREI
S.p. 179 STAPLVRAQTTELKLLKKEVSVNTTKSSSTPSPSTDDN--VPTGTNSLIASGRRVTAEL

S.c. 287 VATERKYVHDLSEHCKYKQQLLSNLITSEELVLFPPNLGDAIDFQRRRLISLEINALWE
K.l. 272 IETERKYVHDLSEHCKYKQQLLSNLITSEELVLFPPNLGDAIDFQRRRLISLEINALWE
C.a. 286 IETERKYVHDLSEHCKYKQQLLSNLITSEELVLFPPNLGDAIDFQRRRLISLEINALWE
S.p. 237 VETERKYVHDLSEHCKYKQQLLSNLITSEELVLFPPNLGDAIDFQRRRLISLEINALWE

S.c. 347 PQORIGALDPSRSHFFLYVFNSTGQNAHIFLESSTLTHWVDEQKRLINNLBLESS
K.l. 332 SQORIGALDPSRSHFFLYVFNSTGQNAHIFLESSTLTHWVDEQKRLINNLBLESS
C.a. 346 IRYORIGSVRIHAGLQPSNAYEPWHICOLTAIDLINKEAANKKSSSE--LDPGPELQSS
S.p. 297 VREORIGSALRIALRR-GEVYQVECTNFFNAQQQLIDNQQLLVANU--LEPSYSLPA

S.c. 406 PLKFPVQRLCRYPLLVRELLARSSDDN-----NTSELBAALDISENTARGINEN
K.l. 390 PLKFPVQRLCRYPLLVRELLARSSDDN-----SKELBIALQDAKSIARNINEN
C.a. 403 YLKEPIQRLCRYPLLVRELLARSSDDN-----YQYRESEKQGMACVYRVANQVNET
S.p. 353 LKIKELQRIQRYPLLVRELLARSSDDN-----YQYRESEKQGMACVYRVANQVNET

S.c. 455 QRTENHGVVKKLVGRVNVWKGVRISKPGELLYFDKQVISTNSSSPEKSPFVYLFKEI
K.l. 437 QRTENHGVVKKLVGRVNVWKGVRISKPGELLYFDKQVISTNSSSPEKSPFVYLFKEI
C.a. 463 QRTENHGVVKKLVGRVNVWKGVRISKPGELLYFDKQVISTNSSSPEKSPFVYLFKEI
S.p. 403 RMTENHGVVKKLVGRVNVWKGVRISKPGELLYFDKQVISTNSSSPEKSPFVYLFKEI

```

FIG. 9C

Homology of Ste4p binding region

```

S.c. 170 PLCILFNSVVKPQCFKLPVIASDDLK---VCKKSIYDFILGCKKHFAFNDEELFTISDVFSN
K.l. 164 PLCIIFNAVVRPQSKLTIVVSSDDIK---ICKKSIYDFILGLKQKHFAFNDEELFTISDVFSN
C.a. 180 PECVLINHHLEDSQIFPVSSDDLK---ICKKSIYDFILGCKKHFAFNDEELFTISDVFSN
S.p. 119 PLCALFNCLPVKQKLEVNSSVSLSENTNVCKASLYRFFMLMCKKNELGLTDAALFSSISBIYKFP

S.c. 227 STSOLVKVLEVVETLMNSSPTIFPSKSKTOQIMNAENQHRHQPQSSKKHNEYVKIIEKF
K.l. 221 STDHFLKVLVDVNTLLNAAEVEFPQIDMSTOLE-----S-QRAKAPQTEYDKIVKEF
C.a. 237 NAQDLIKIIVINKLLAEVSDASDGGGDEDVN-----MDVQITDERSKVFPREI
S.p. 179 STAPLVRAQTTELKLLKKEVSVNTTKSSSTPSPSTDDN--VPTGTNSLIASGRRVTAEL

```

FIG. 9D

Homology of Bem1p binding region

```

S.c. 774 -----NTSSSEIFTLLVEKVVNFDDLLIMAINSKISNTHNNNI-S-PTIKIKYQD
K.l. 789 -----DFYTVLVSLDCSAEDLLLAIKRKLHLG-----VITKVKYQD
C.a. 746 TFD--VAIKLLYKSTELSEPLIVNAQIEYNDLLQKIIISQITSNLVADDV-NISRLRYKD
S.p. 768 SVRNTTNVKIRLRLHEVSLVLVVAHDTFEDELLAKVEBKIKLCGILKQAVPFRVRLKYVD

S.c. 822 EDGDFVVLGSDDEDWVAKEMLA-----ENNEKFLNTRY---
K.l. 723 EDGDFVMLESDDDWVVKDMLK-----ESNERLLNVW---
C.a. 804 DEGDFVNLNSDDDWGLVLDMLTSEDIFYQTSSNEKRSVTVVVS---
S.p. 828 EDGDFITTTSDDEDVLMAFETCTFELMDPVHNKGMDTVSLHVVVYP

```



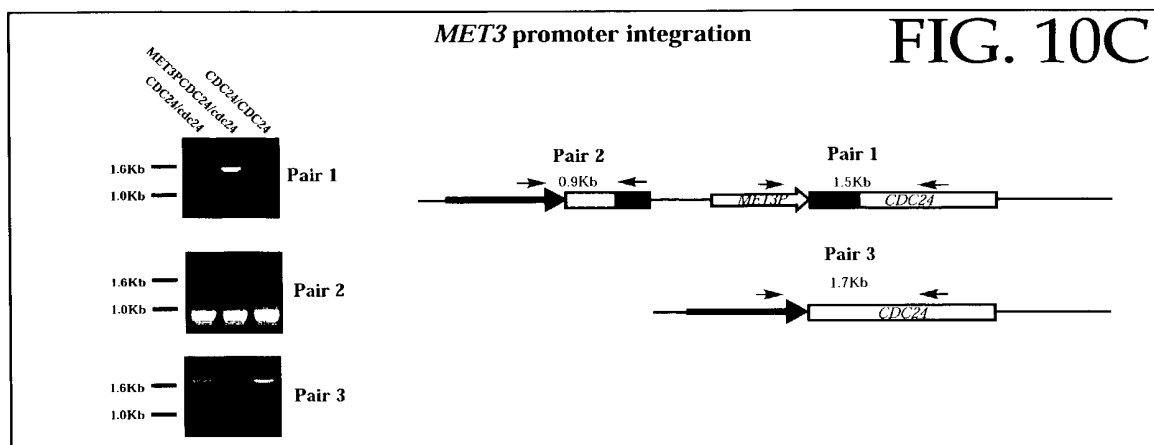
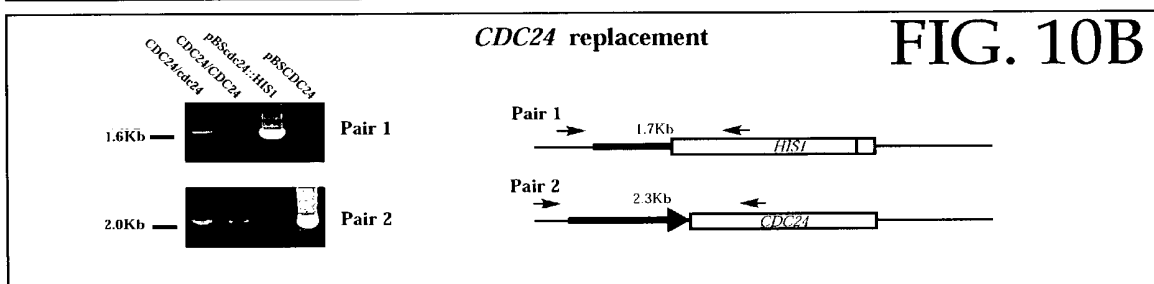
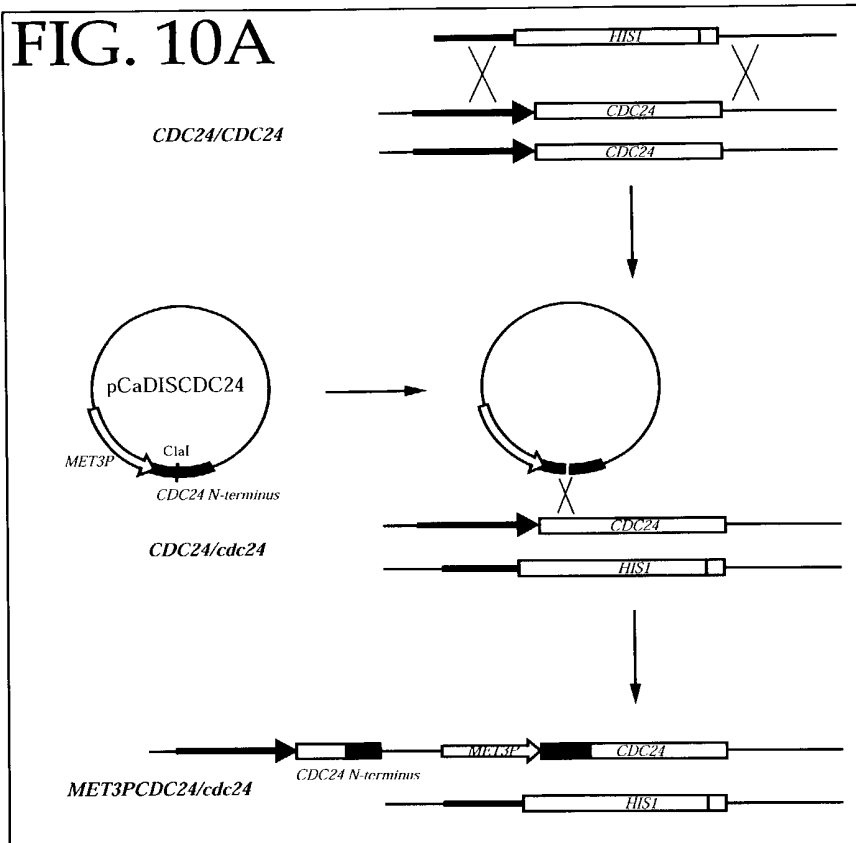

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FIG. 11A

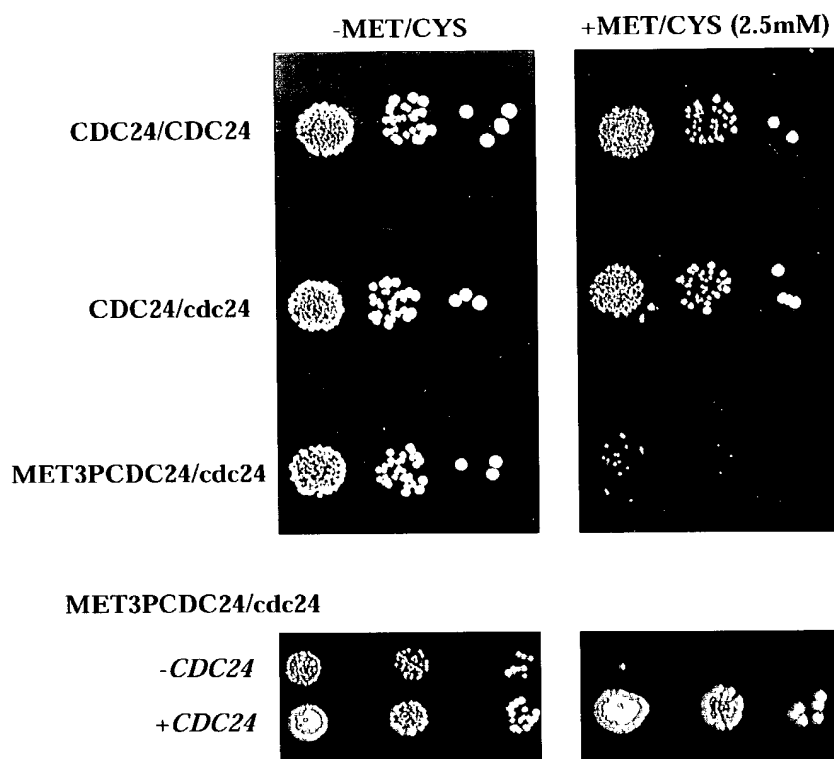


FIG. 11B

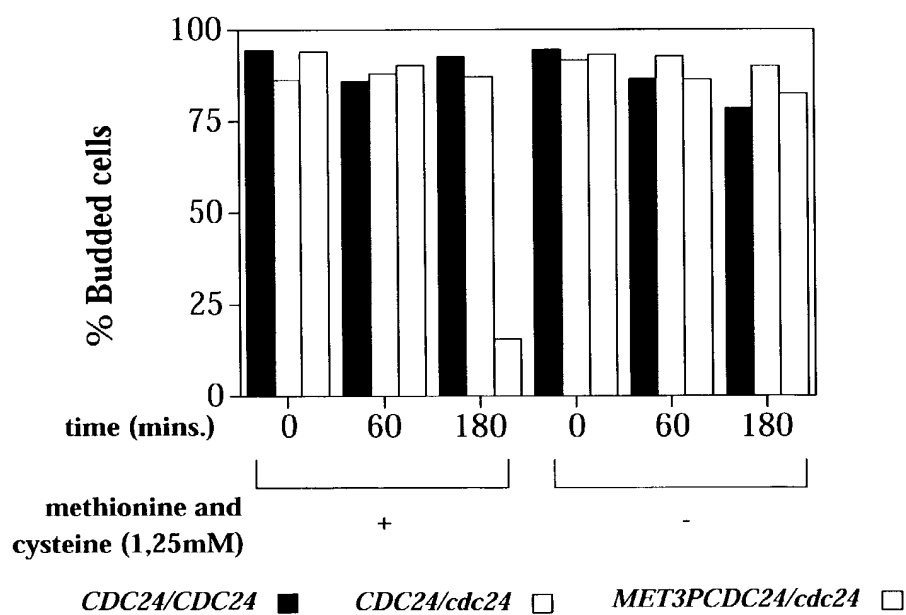


FIG. 12A

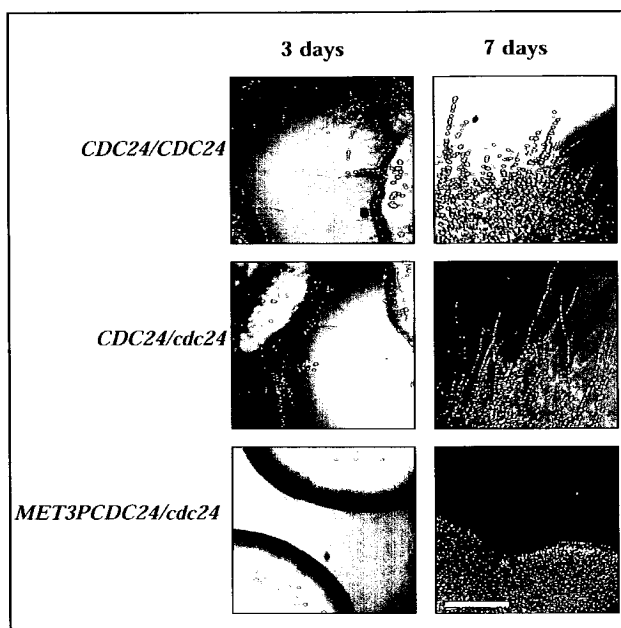


FIG. 12B

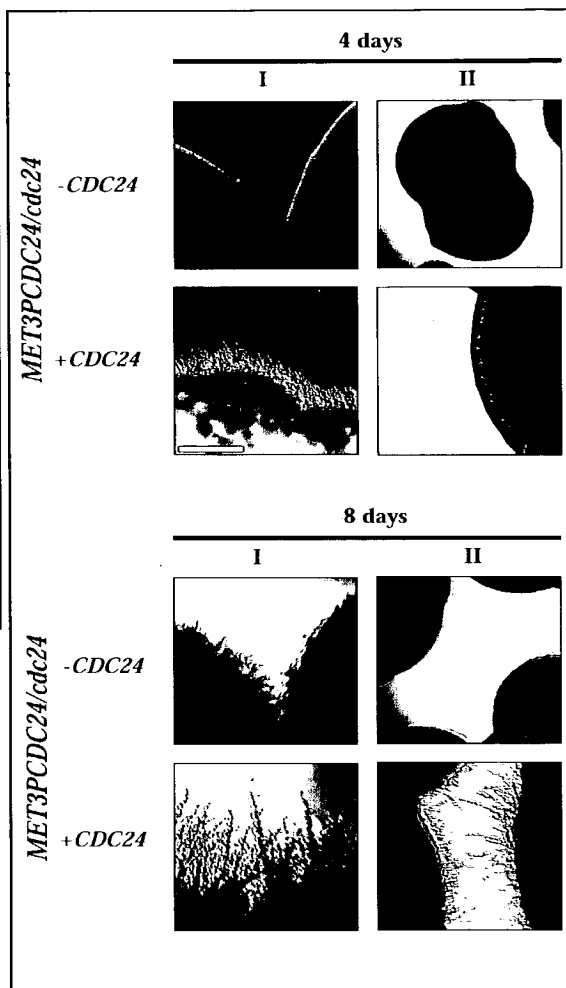
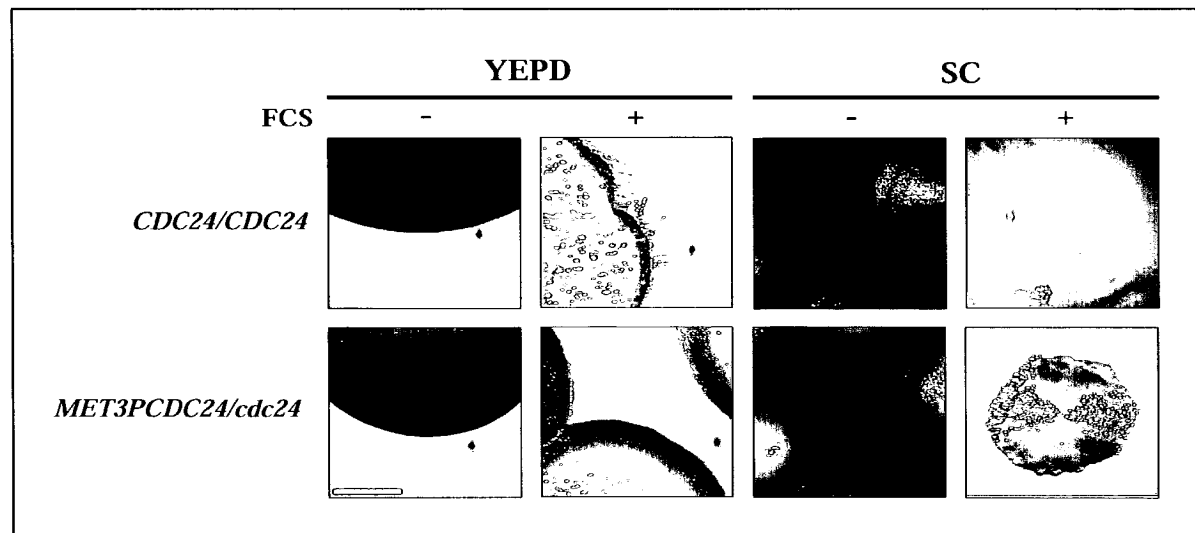


FIG. 12C





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FIG. 14A

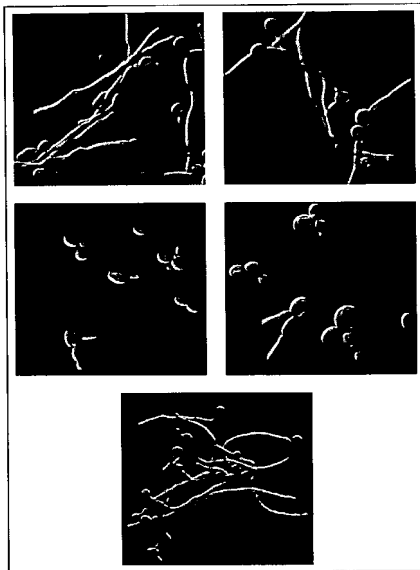


FIG. 14B

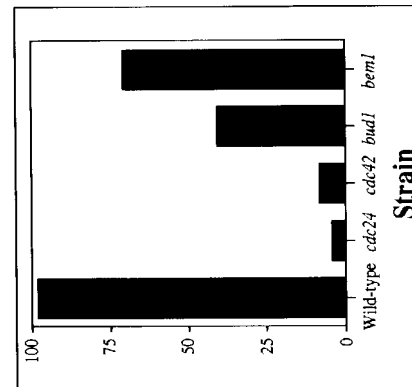


FIG. 13A

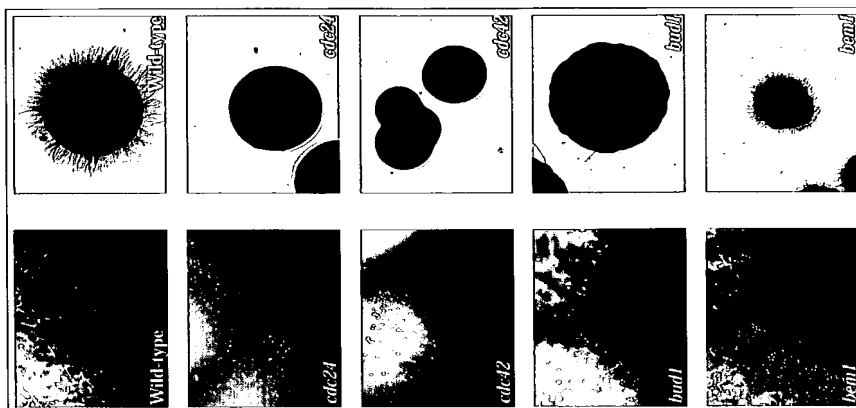


FIG. 13B

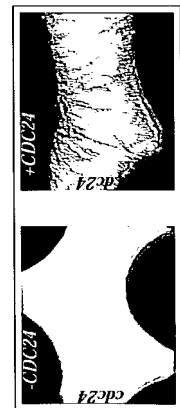




FIG. 15A

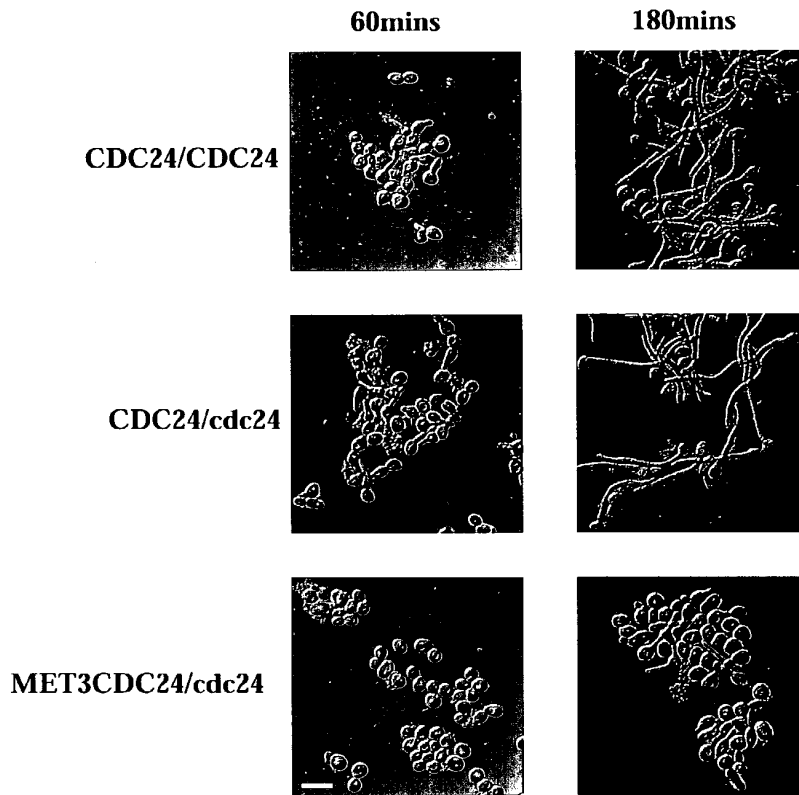
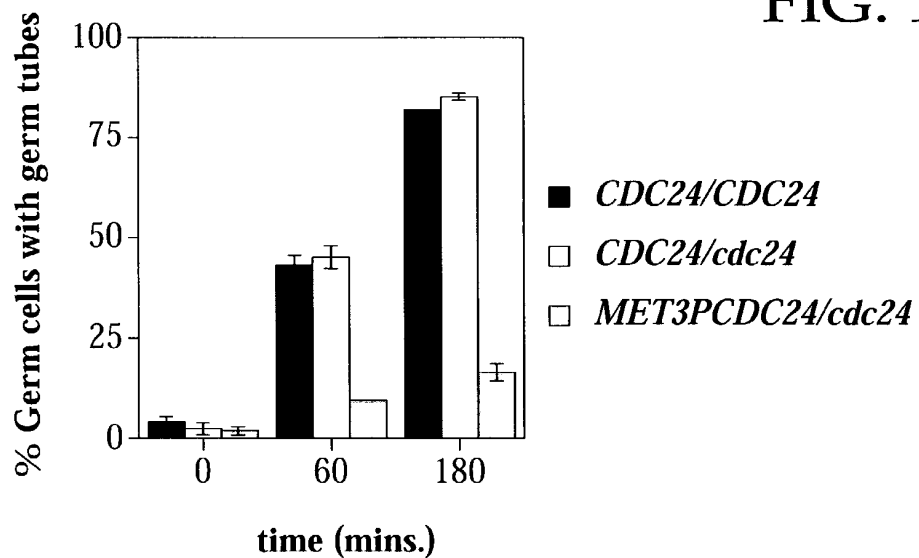


FIG. 15B





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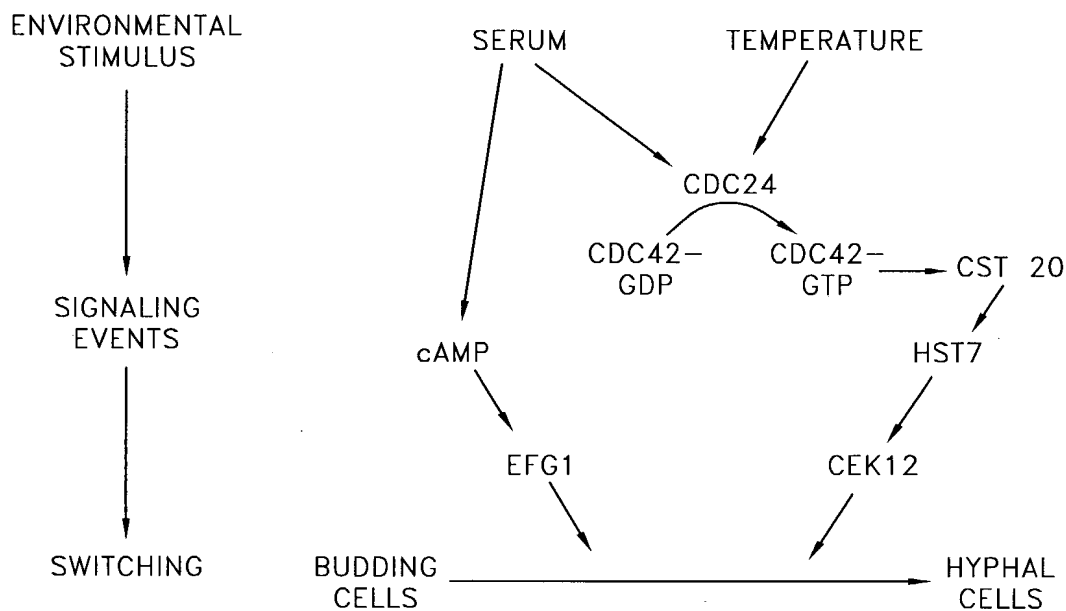


FIG. 16



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FIG. 17_A

FIG. 17_B

FIG. 17_C

FIG. 17_D

FIG. 17_E

FIG. 17



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A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatctgacgattgaaagtctgtaaaaatccatttatgactt
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatttgacgattgaaagtctgtaaaaatccatttatgacttt
atattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

30

FIG. 17_A



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FIG. 17_B

C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatctggcgatttgaaagtctgtaaaaatccatttatgactt
tatattgggctgcaagaaacactttgcatttaacgatgaggagcttttcactatatccgacgtttttgccaaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 cccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcacctgacgatttgaaagtctgtaaaaatccatttatgactt
tatattgggctgcaagaaacactttgcatttaacgatgaggagcttttcactatatccgacgtttttgccaaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVIAPDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEV VETLMNSS

NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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FIG. 17c

SEQ ID NO. 10

STE4 DNA sequence (wild-type)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
TATCTCTGCAGTGGAGGAAGAAATTCAAAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATAA
ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCAGATGGCCAACAAAGTTACTTCGTTGACCAAAAATAAGATC
5 AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTAT
TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGATT
CTCAATGGGTTCTTTCCTGCGCTATTTGCGCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT
TATAGAGTTTCGAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAGA
10 GGGTGAGAGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAACTTAGAAAATTCTTCG
AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCCGCTGTACAAAGCTTTTA
CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCGA
TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTCGAGGTTATGAAGACGTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAAATCAACAAGCTCAAGCTATCT
15 AGACAACCAAGCGTGTGTTTCTTTAGATTTTAGTGATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTAAGAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

20 SEQ ID NO. 11

Ste4 Protein sequence (wild-type)

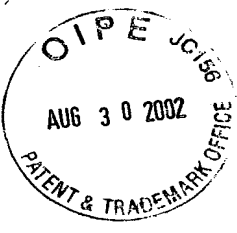
MAHQMDSITYSNNVTQQYIQPQSLQDISAVEEEIIONKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKIN
LKPNIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNNNCTIY
25 RVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDHLGDVLAALAIPEEPNLENSN
TFASCGSDGYTIWDSRSPSAVQSFYVNSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPTP
TYMAANMEYNATAQSPQTLKSTSSSYLDNQGAVSLDFSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRSSP
DGLAVCTGSWDSTMKIWSPGYQ

30

SEQ ID NO. 12

ste4-o15 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
35 TATCTCTGCAGTGGAGGAAGAAATTCAAAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATAA
ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCAGATGGCCAACAAAGTTACTTCGTTGACCAAAAATAAGATC
AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTAT



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

Nern et al.

Appl. No.: 10/054,399 Atty Docket: DYOU13.1A2CPI

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FIG. 17_D

TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGATT
CTCAATGGGTTCTTTCTGCGCTATTTGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAACAATAACTGTACCATT
TATAGAGTTTCGAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAGA
5 GGGTGAGAGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAAACTTAGAAAATTCTTCG
AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCCGCTGTACAAAGCTTTTA
CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCGA
TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTTCGAGGTTATGAAGAAGCTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATGCCACAAACTTTAAATCAACAAGCTCAAGCTATCT
10 AGACAACCAAGGCGTTGTTTCTTTAGATTTTAGTGCATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTAAGAGAGAGATTGTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

SEQ ID NO. 13

15 Ste4-ol5 Protein sequence (mutant)

MAHQMDSITYSNNVTQQYIQPSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKIN
LKPNIIVLKGHNNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNNCTIY
RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDDLGLDLALAIPEEPNLENSN
20 TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPTP
TYMAANMEYNATAQSPQTLKSTSSSYLDNQAVSLDFSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRSSP
DGLAVCTGSWDSTMKIWSPGYQ

SEQ ID NO. 14

25 ste4-ol7 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGCTACAGGA
TATCTCTGCAGTGGAGGAAGAAATTCAAAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATAA
ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCAACAAAGTTACTTTCGTTGACCAAAAATAAGATC
30 AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTAT
TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGATT
CTCAATGGGTTCTTTCTGCGCTATTTGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAACAATAACTGTACCATT
TATAGAGTTTCGAAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAGA
35 GGGTGAGAGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAAACTTAGAAAATTCTTCG
AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCCGCTGTACAAAGCTTTTA
CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCGA



NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

Nern et al.

Appl. No.: 10/054,399 Atty Docket: DYOU13.1A2CP1

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FIG. 17_E

TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTTTCGAGGTTATGAAGAACGTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAAATCAACAAGCTCAAGCTATCT
AGACAACCAAGGCGTTGTTTCTTTAGATTTTAGTGCATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTTAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
5 CCAGATGGGTTAGCTGTATGTACAGGTTGATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

SEQ ID NO. 15

Ste4-ol7 Protein sequence (mutant)

10 MAHQMDSITYSNNVTQQYIQPSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKIN
LKPNIIVLKGHNNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNNCTIY
RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDDLGLDVLALAIPEEPNLENSN
TFASCGSDGYTYIWDSRSPSAVQSFYVNSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPTP
TYMAANMEYNTAQSPQTLKSTSSSYLDNQAVSLDFSASGRMLYSCYTDIGCVVWDLKGEIVGKLEGHGGRVTGVRSSP
15 DGLAVCTGSWDSTMKIWSPGYQ

SEQ I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly".

SEQ I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ I.D. No:22 refers to peptide sequence "QYEFDVILSPELKVQMKTII".